

RESULT 1
CEZK945 27981 bp DNA INV 06-SEP-1999
LOCUS Caenorhabditis elegans cosmid ZK945, complete sequence.
DEFINITION Z48544
ACCESSION GI:695493
VERSION 1
KEYWORDS HTG; ARD1; Esterase; Mucin; Polycystic kidney disease protein 1;
Proteasome component(A-type); Pumilio.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
Rhabditina; Rhabditoidae; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 27981)
Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M.,
Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J.,
Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A.,
Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M.,
Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N.,
Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B.,
O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A.,
Saunders, R., Snowkneen, R., Smaildon, N., Smith, A., Sonnenhammer, E.,
Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M.,
Vaughan, K., Waterston, R., Watson, A., Weinstein, L.,
Wilkinson-Sprat, J. and Wohldman, P.
2-2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans
2 (bases 1 to 27981)
Submitted (01-MAR-1995) Louis, MO 63110, USA. E-mail:
jes@sanger.ac.uk or tw@nematode.wustl.edu
Coding sequences below are predicted from computer analysis, using
predictions from Gensfinder (P. Green, U. Washington), and other
available information.
For a graphical representation of this sequence and its analysis
see:-
http://webace.sanger.ac.uk/cgi-
bin/display?db=wormace&class=Sequence&subject=ZK945
Current sequence finishing criteria for the C. elegans genome
sequencing consortium are that all bases are either sequenced
unambiguously on both strands, or on a single strand with both a
dye primer and dye terminator reaction, from distinct subclones.
Exceptions are indicated by an explicit note.
IMPORTANT: This sequence is NOT necessarily the entire insert of
the specified clone. It may be shorter because we only sequence
overlapping sections once, or longer because we arrange for a small
overlap between neighbouring submissions.
IMPORTANT: This sequence is not the entire insert of clone ZK945.
It may be shorter because we only sequence overlapping sections
once, or longer because we arrange for a small overlap between
neighbouring submissions.
The true left end of clone ZK945 is at 1 in this sequence. The true
right end of clone ZK945 is at 8882 in
sequence Z48582.
The true left end of clone F27E5 is at 27881 in this sequence. The
true right end of clone C18D1 is at 2079 in this sequence. The
start of this sequence (1..104) overlaps with the end of sequence
Z48543.
The end of this sequence (27881..27981) overlaps with the start of
sequence Z48582.
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Mon May

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Db	22480		ATGCTGAGCTTAAGTTGAAACCAATTAACCTCTCCRAACCAATCTTTCTTACCGTACAC	22539
Qy	6781	ctaggcgataccaatgtatatacccgatgcaataacaatatccaaaaataaacccgtaagtt	6840	
Db	22540	CTAGCGATACCAATGTATATCCCGATGCAATAACATATCCAAAAATAACCGCGTAAGTT	22599	
Qy	6841	ccatctttgattttgtaactgtatactcccgaaggtatagaactgtactctctttgagagca	6900	
Db	22600	CCATCTTTTGTATTTGTACTTGTATCTACCTCCCAAGGTATAGACTGTACTCTCTTTCAGAGCA	22659	
Qy	6901	agatcgagagagacagtcacggagttcaagagttgtcggaagtcataattgacatttgct	6960	
Db	22660	AGATCGAGAGAAGACAGTACGGAGTTCAAGGATTTGCGGAAGTCATATTGACATTGCT	22719	
Qy	6961	agtttagtgataaacttttgccatttcgtcggaattccgaatttgttgttgcaaatatcg	7020	
Db	22720	AGTTTAGTGATAACTTTTGCCATTTCTGTGCGCCAAATTCGGAATTTGTGTGTGCAATATTG	22779	
Qy	7021	ctctgcaatgttttcaaaacatacaacttgacatatattccgactccagggtatttgagg	7080	
Db	22780	TCTTGCAATGTTTCAAAAACATCAACACTTGACATATTTCCGACTCCAGGGAATTTGAGG	22839	
Qy	7081	gtatttgagagcaaaactttgagcaacttccactagatatcgtcggcaggtagagatgagatt	7140	
Db	22840	GTATTTGAGAGCAAACTTTGAGCAACTTCCACTAGATCTCGCGGAGGTAGAGATGAGATT	22899	
Qy	7141	tgattgagaagagagctgctgtgttttagagagttgttgatcgagatcccatcattatc	7200	
Db	22900	TGATTGAGAAAGAGAGCTGCTTGTTTAGAGAGTTGTGGATGAGATCCCATTCATATC	22959	
Qy	7201	ccagccagttggttcattacatcacgctttttgagcatctatgctgcgtgttccagctgca	7260	
Db	22960	CCAGCCAGTTGGTTCATTACATCAGCTTTTGGAGCATCTATGATCGCTGTGTCAGCTGCA	23019	
Qy	7261	gaattgggagaaactgtgtgcaagagagctgcgagtttagtagttcttctgtagatggttgc	7320	
Db	23020	GAATTTGAGAGAAACTGTTTGCAAGAGAGCTGCGAGTTTGTAGTGTCTGTAGATGGTTGC	23079	
Qy	7321	gcggtagcagagaatgcaccatttgcaccagagaatcggaagatccagacgctatcgag	7380	
Db	23080	CGGTAGCAGAGATGCAACATTTGCACCAGAGAAATCGGAAGATCCAGACGTATCGGAG	23139	
Qy	7381	ccagatgagctcttggttgaaacaccagaagaatccattgtaattgatctctgagccagat	7440	
Db	23140	CCAGATGAGCTCTTGGTTGAAACACCAAGAGATCCATTTGAAATCTGATCCTTGAGCCAGAT	23199	
Qy	7441	gtaatacacgctctcctaataatggatcctgtgtgtgtagctgttccagatccctgtacca	7500	
Db	23200	GTACTACACCGCTCTCTTAATGGATCTCTGGTGTGGTAGTGTGTCCAGATCCTGTACCA	23259	
Qy	7501	tctccattcaatgcgctgtttttccagagtttaccgcgtccgaacccgctccctgaagac	7560	
Db	23260	TCTCCATTCAATGCGTTGTTTTCCAGAGTTTACCOCGTCCGAACCGTCCCTGAAGAC	23319	
Qy	7561	ccccctgaccacttccaagagcggtggttctctgatccaacagcccccgatcccggtgat	7620	
Db	23320	CCCGCTGACCACATTCAGAGACGGTCTGCTCTGATCCACACGCCCCGATCCCGTTGAT	23379	
Qy	7621	gattgtccacttccagatccgaagtggttgatctgactgcatcaccccgctctaagagtt	7680	
Db	23380	GATGTCCACTTCCAGATCCAGAGAGTGGTGTGATCTGACTGCATCACCCTGCTAAGAGTT	23439	
Qy	7681	gtcgagatcctctgaaacctgttccaccagtctccccagtagctccagttccaccggctt	7740	
Db	23440	GTCGCAGATCTCTGTAACTGTTTCCACAGTGTCCCCAGTAGTCTCCAGTTCACCGGTT	23499	
Qy	7741	tgcacacgcatcatccgacgcactgacagtggtgtgggtttctcaaaattgcaatt	7800	
Db	23500	TTGCCACCGGCATCATCCGACAGCTGACAGTGGTGTGTGGGGTCTCTAATAATTCAATT	23559	
Qy	7801	ttatgaaaaaaaacagtaatgcgcttaccagtagttgtagtttggaagaactacattcat	7860	

